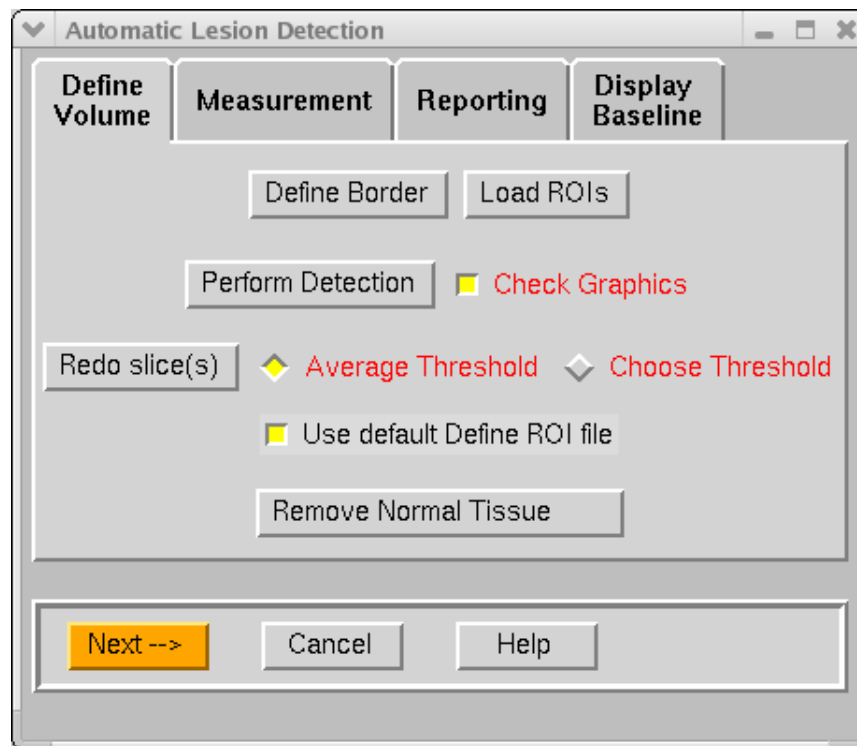


## **Automatic Lesion Detection (ALD) Application**

The automatic lesion detection application was initially developed to measure the volume of plexiform neurofibroma lesions in STIR MRI scans for patients with NF1 disease. In these scans, the lesion is hyper-intense with respect to surrounding normal tissue. This is a semi-automated segmentation which requires a rough manual tracing before the automated aspect of the segmentation occurs. The volume is saved in a report and has been used to track the progression of lesions over time in patients during clinical drug trials. This application has been included in MEDx in the hopes that it can be applied to other situations where hyper-intense lesions are visible on MRI images.

To run the Automatic Lesion Detection application, choose **Automated Body Lesion Detection** option under the **Volumetric** menu in the toolbox. The following User Interface will appear.



**Figure 1**

As can be seen in Figure 1, there are four main tabs corresponding to four high level functions of this program. These tab labels include *Define Volume*, *Measurement*, *Reporting* and *Display Baseline*. When analyzing the hyper-intense lesions, the workflow goes from left to right. In other words, the user will *Define* the *Volume* of the lesion semi-automatically (this is the heart of the program), then perform the volumetric *Measurement* and then save the *Reporting* results to a file. Finally, one may *Display* the *Baseline* sessions for comparison with previous studies.

This document will describe the purpose of each option (button selection) found under the four main tabs of the Automatic Lesion Detection program. While using this document to learn this tool, please only interact with the program when you see the indented lines starting with the word **Step:** . While all of the features of this application are described, due to the many options available, not all will be executed in this document.

### **Define Volume**

*Define Border:* This option allows the user to define a region of interest that should include the entire lesion on a slice as well as some amount of normal tissue. Ideally, the area of lesion should be roughly the same as the area of normal tissue. Defining the Border is the first step in the lesion detection process.

**Step 1:** Select New Folder under the File menu and use the Open Image dialog box to open the MR image named \$PXHOME/images/tutorials/pn.hdr.

**Step 2:** If you have not yet started the Automatic Lesion Detection program by selecting Automatic Body Lesion Detection from the Volumetric menu in the toolbox, do so now.

**Step 3:** In the Automatic Lesion Detection program, select the Define Border button. You will be prompted to trace the regions which include both lesion and normal tissue, then select the OK button. Scroll down to slice 7 and trace the lesion as depicted in Figure 2. Similarly, trace the lesion in slices 6, 8 and 9 with the goal of excluding the eye and including some normal tissue. Finally select the OK button in the Script Pause window.

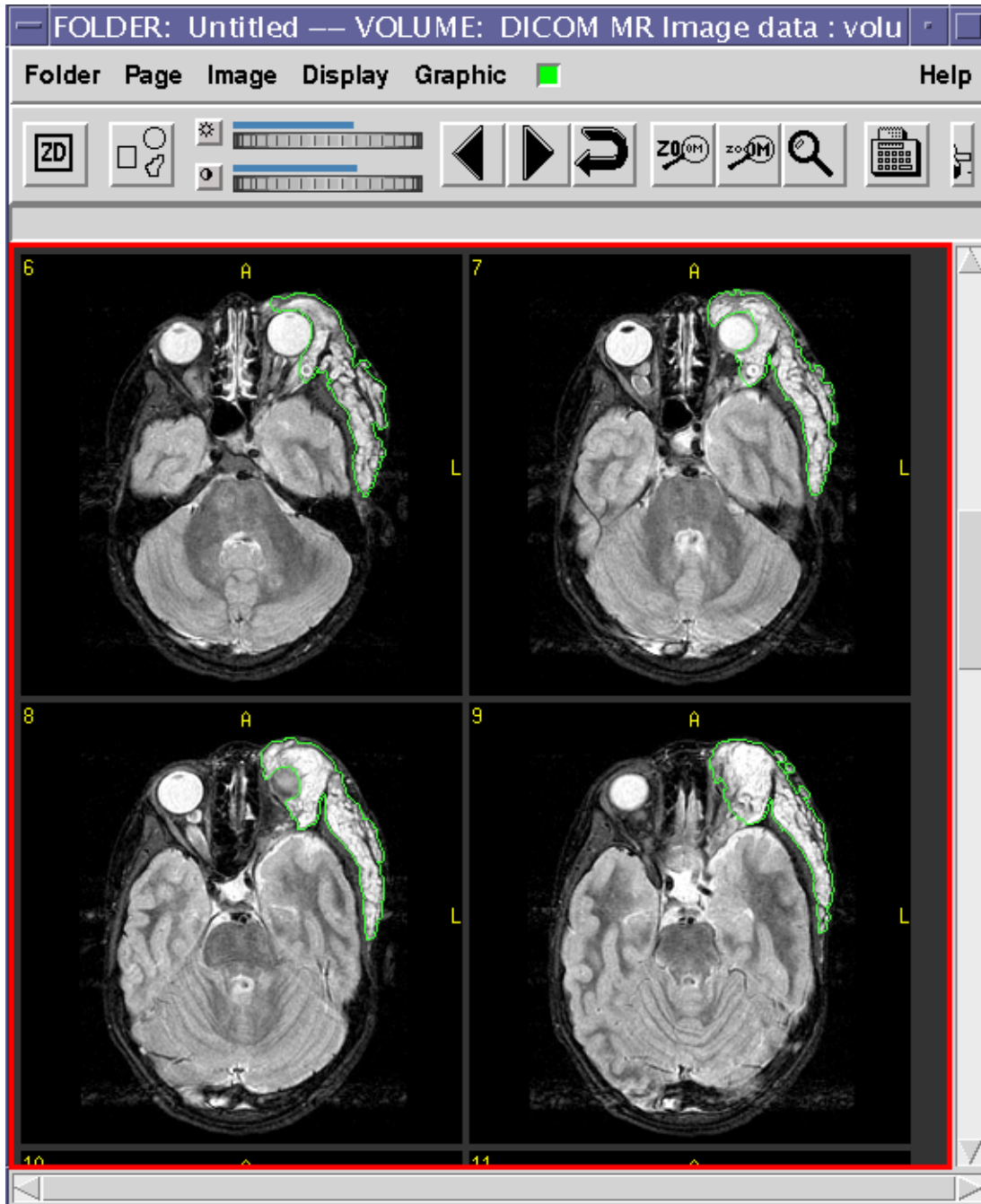


**Figure 2.** Shows an example of a lesion with the border roughly defined in this manner. This operation is performed on all slices that contain the lesion.

**Step 4:** You will be prompted for the File Name to be used when saving the border roi. Choose /tmp/border.roi. After selecting OK, the areas outside of the border roi are deleted.

**Step 5:** Select the *Perform Detection* button. Selecting this option will initiate the automated aspect of this lesion detection program. You can leave the *Check Graphics* button (located next to the *Perform Detection* button) selected as this is used to automatically confirm that the correct number of resulting graphics are drawn. The user will be prompted to enter a Slice Range (Lower Slice # and Higher Slice #). The lesion should extend across this slice range. Enter 6 and 9 for the Lower and Higher slice numbers and then select OK. For each slice within the slice range, a histogram will be computed. Analysis of this histogram will derive a threshold value used to segment out non-lesion tissue. An edge enhancement operation is performed, along with a connected component analysis to get rid of false positives too small to be lesions, and finally a

contour around the lesion is created. The user must wait until this process is completed on all slices. Figure 3 shows the resulting contours automatically placed on the volume.



**Figure 3.** Final ROIs appear on top of each slice containing the lesion.

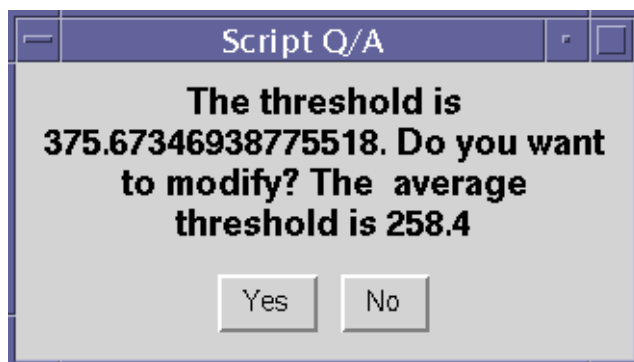
*Load ROIs:* This option allows the user to load a saved set of ROIs. While any saved ROI can be loaded, in most cases this option will be used to load ROIs that have been previously used on the image of interest to define the border of the lesion.

**Step 6:** Once the Perform Detection process has been completed, the user should inspect the contours that were automatically created. In the case where one or more contours do not accurately estimate the boundary of the lesion, the *Redo Slice(s)* option may be invoked. Select the button labeled Redo Slice(s) and enter the 9, when prompted for the slice selection as shown in Figure 4.

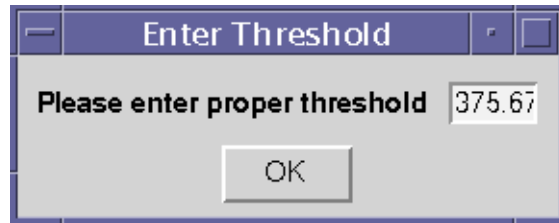


**Figure 4**

There is currently no option to enter a range such as 6-9. As can be seen in Figure 1, the user has the choice of having the program use the *Average Threshold* from all slices automatically, or can select the *Choose Threshold* option, which will allow the user to interactively adjust the threshold value for each slice. When the *Choose Threshold* option is selected, the user is prompted with the Average Threshold as well as the histogram computed threshold. The user may choose either of these values or enter their own based on some a priori knowledge. For instance, if the computed threshold seems too high (too much lesion is automatically discarded during the threshold process), a lower value may be entered. This option is seen in Figures 5 and 6 below.



**Figure 5**



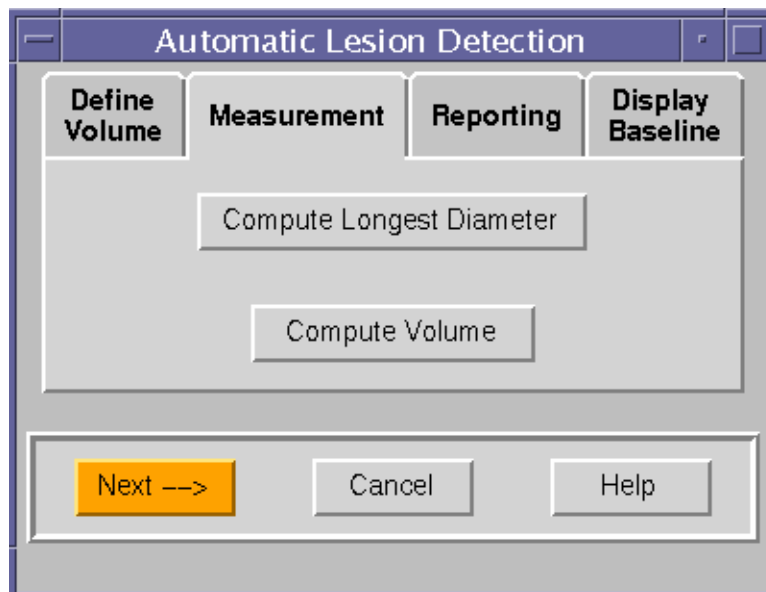
**Figure 6**

Another option available when in Choose Threshold mode is to automatically *Load the Border ROIs* or to *Re-draw the Border ROIs*. This option is available for the case when the previously drawn border ROIs need to be re-drawn.

*Remove Normal Tissue:* In rare cases, normal tissue may be included inside the automatically created contour. If this is the case, the user may choose the *Remove Normal Tissue* option. The user will be prompted to draw an outline of the normal tissue that he/she wishes to remove from the volume calculation. If the tissue is normal and not plexiform neurofibroma, it should not contribute to the total lesion volume. The user must draw an outline on all slices where there is normal tissue inside a lesion contour. Once complete, pixel values inside the drawings will have value 0 and will not contribute to the lesion volume calculation.

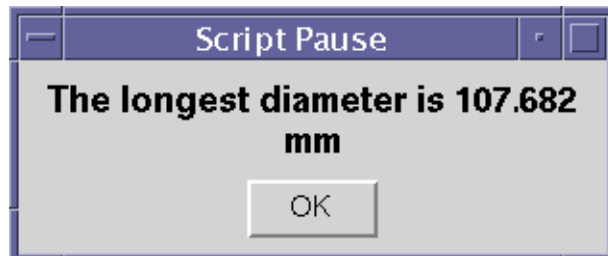
### **Measurement**

This network tab, seen in Figure 7 below, is used for calculating lesion measurements.



**Figure 7**

*Compute Longest Diameter:* This option is available if the user wants to measure the longest diameter of the lesion in a chosen slice. Normally, this option is not used, but has been made available for those who wish to compare the volumetric results with the longest diameter measurement conventionally used. The user will be prompted to select the graphic on the slice to compute the longest diameter. Once selected, the longest diameter of the lesion on the selected slice is displayed as in Figure 8.



**Figure 8**

In addition, a line graphic showing the longest diameter is displayed on the chosen slice.

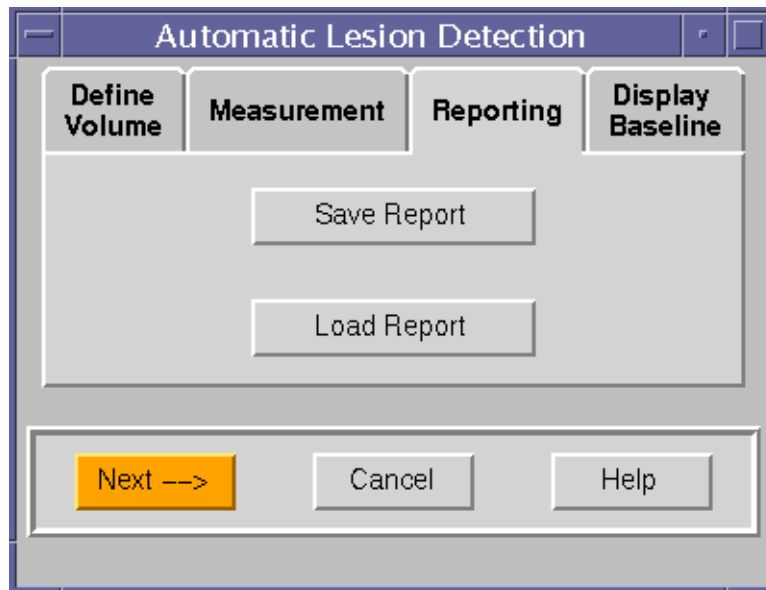
**Step 7:** Select *Compute Volume* to compute the total volume of the lesion. There is no further user interaction; the results are simply displayed as seen in Figure 9. This result is later saved in a report. See **Reporting** notebook tab description.



**Figure 9**

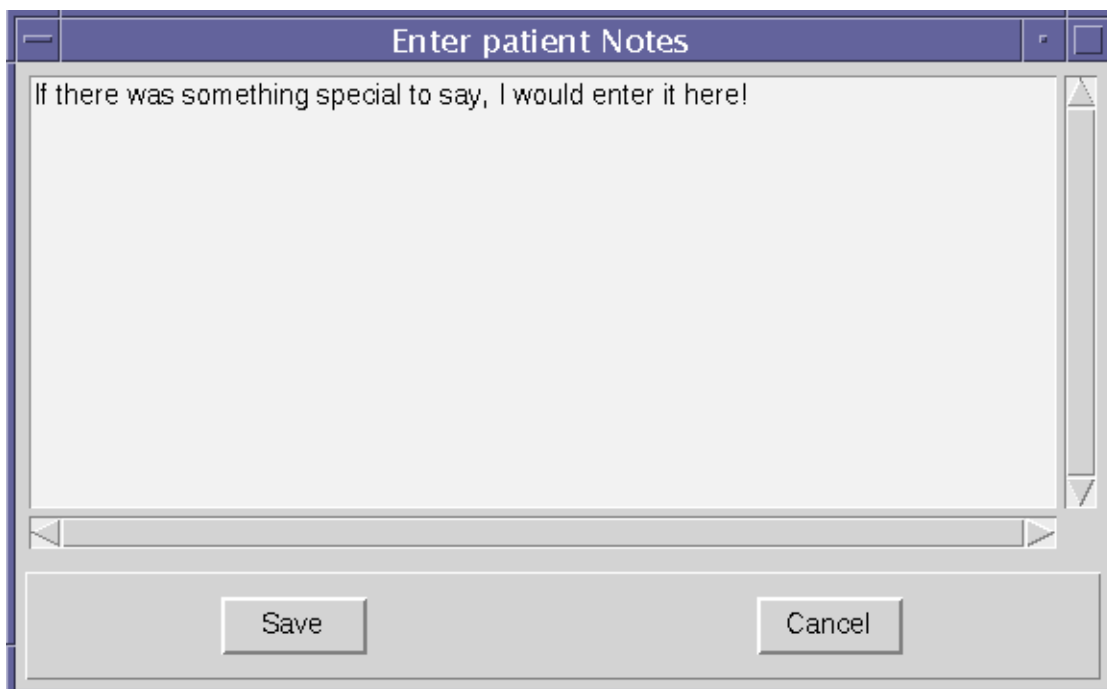
## **Reporting**

As can be seen in Figure 10, this tab is used to save and optionally load a report that was previously saved.



**Figure 10**

**Step 8:** Select *Save Report*. This option is used to save the volumetric measurement as well as a report of all thresholds used in the automatic detection process. The lesion contours are automatically saved with this report. You will be prompted to enter optional patient notes (Figure 11).



**Figure 11**



A report file name must be entered. By default, it has a similar name to the input image and will be stored in the same UNIX directory as the input image and defined ROIs. After typing something into the optional patient notes, enter the full path and file name of a report file (e.g. /tmp/report) and select OK in the File Name window.

*Step 9:* Select the *Load Report* button. This option is used to display the volumetric results as well as to load the automatically created contours, which define the lesion. By default, the report file path and name that was entered in step 8 is displayed. Select the *Load* button. The volumetric results and threshold values used are displayed in a web browser as seen in Figure 12.

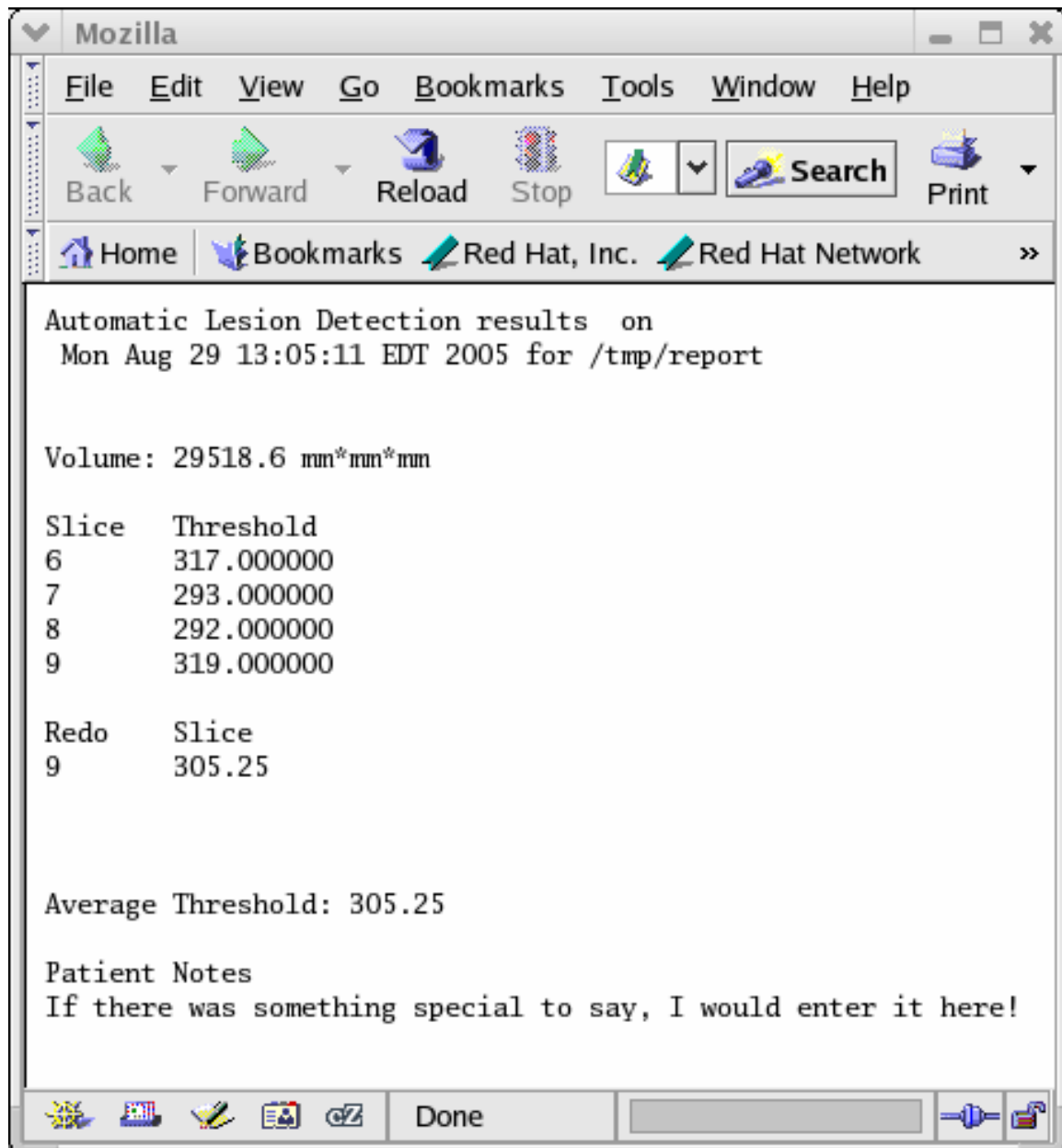


Figure 12

## **Display Baseline**

This tab is used to open a previously analyzed image of the same patient (Baseline Image). The report for this previous study may be displayed and compared with the current study being analyzed. These options were made available so that the user could improve the measurement of the current volume based on previous results for this subject. There is no intent to bias the automated algorithm, but to aid in the process. An example would be to improve the process of roughly defining the borders of the lesion.

*Open Baseline Image:* Selecting this option will cause a new MEDx folder to be created and the user will be prompted to load the baseline volume. Once selected, this volume will be displayed in a folder. The current study being analyzed will still be displayed in a separate folder next to the baseline image folder.

*Load Report:* This option is the same as in the Reporting tab, but this time the contours are displayed on the baseline image and the report references this baseline image.